AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning on page 8, line 11 with the following paragraph:

SEQ ID NOs: 25-~~38~~ 53 are oligonucleotide sequences that overlap the intron-exon boundaries in the human *Mater* gene. In order, these oligonucleotides correspond to the splice junctions that define exons 1-15, as described more fully herein.

Please replace the paragraph beginning on page 8, line 14 with the following paragraph:

SEQ ID NOs: ~~39~~ 54 and 55 ~~40~~ are human β-actin specific primers.

Please replace the paragraph beginning on page 8, line 15 with the following paragraph:

SEQ ID NOs: ~~41~~ 56 and 57 ~~42~~ are human MATER-specific primers.

Please replace the paragraph beginning on page 20, line 32 with the following paragraph:

Another embodiment is a method of detecting in a subject a biological condition associated with an abnormal *MATER* nucleic acid, which method involves reacting at least one *MATER* nucleic acid in a clinical sample from the subject with a reagent comprising a *MATER*-specific nucleic acid binding agent to form a *MATER*:agent complex, and detecting the complex. In specific examples of this method, the *MATER*-specific nucleic acid binding agent is a *MATER* oligonucleotide, for instance one that comprises at least 10 contiguous nucleotides of a human *MATER* intron sequence. By way of example, certain of the *MATER* oligonucleotides include a sequence as shown in any one of SEQ ID NOs: 25 through ~~38~~ 53.

Please replace the paragraph beginning on page 21, line 9 with the following paragraph:

Representative examples of provided methods of detecting in a subject a biological condition associated with an abnormal *MATER* nucleic acid further comprising *in vitro* amplifying a *MATER* nucleic acid prior to detecting the abnormal *Mater* nucleic acid. The *in vitro* amplification can be carried out *in vitro* using at least one oligonucleotide primer derived from a MATER protein encoding sequence. Specific examples of the oligonucleotide primer include a sequence of an intron-exon boundary of human MATER, for instance as shown in any on of SEQ ID NOs: 25 through ~~38~~ 53. Other embodiments are oligonucleotide primers used in any of these methods.

Please replace the paragraph beginning on page 21, line 16 with the following paragraph:

In certain examples of the described methods, the *MATER*:agent complex is detected by nucleotide hybridization. The agent, used to form the *MATER*:agent complex in some of the described methods, is a labeled nucleotide probe. Representative examples of such probes include a sequence as shown in any one of SEQ ID NOs: 25 through ~~38~~ 53. Other embodiments are labeled nucleotide probe used in any of these methods.

Please replace the paragraph beginning on page 21, line 21 with the following paragraph:

A further embodiment is a kit for detection of a genetic mutation in a sample of nucleic acid. One such kit includes a first container containing an oligonucleotide capable of specifically hybridizing with a *MATER* nucleic acid, which oligonucleotide has a sequence comprising at least 10 contiguous nucleotides from an human MATER intron; and a second container containing a fluorescent labeled nucleic acid probe that is fully complementary to the oligonucleotide. In examples of these kits, the fluorescent labeled nucleic acid probe has a length of between 5 and 500 nucleotides. Specific examples of kits provided herein include an oligonucleotide that includes a sequence as shown in any one of SEQ ID NOs: 25 through ~~38~~ 53.

Please replace the paragraph beginning on page 31, line 32 with the following paragraph:

As a control, as shown in figure 8B, the PCR products (640 base pairs) of human β-actin were amplified in all cDNA derived from 25 tissues and human ovary (lanes 1-25) using the human β-actin-specific primers (5'-GCATGGGTCAGAAGGAT-3'/3'-GTCCAGTAGTGGTAACC'5'; SEQ ID NOs: ~~39~~ 54 and 55 ~~40~~). In contrast, using human MATER -specific primers, (5'-TGACTTCTGATTGCTGTGAGG-3'/3'--CTACTGGCCATGACCACCTT-5'; SEQ ID NOs: ~~41~~ 56 and 57 ~~42~~), the PCR products (280 base pairs) were only generated in the cDNA synthesized from the ovarian RNA (Figure 8C, lanes 17 and 25).

Please replace the paragraph beginning on page 41, line 11 with the following paragraph:

With the sequences of human *MATER* cDNA and gene in hand, primers derived from these sequences may be used in diagnostic tests (described below) to determine the presence of mutations in any part of the genomic *MATER* gene of a patient. Such primers will be oligonucleotides comprising a fragment of sequence from the *MATER* gene (intron sequence, exon sequence, or a sequence spanning an intron-exon boundary) and may include at least 10 consecutive nucleotides of the *MATER* cDNA or gene. Specific examples of such oligonucleotides include those comprising the sequences shown in SEQ ID NOs: 25-~~38~~53. It will be appreciated that greater specificity may be achieved by using primers of greater lengths. Thus, in order to obtain enhanced specificity, the primers used may comprise 15, 17, 20, 23, 25, 30, 40 or even 50 consecutive nucleotides of the *MATER* cDNA or gene, particularly overlapping an intron-exon boundary. Furthermore, with the provision of the *MATER* intron sequence information, the analysis of a large and as yet untapped source of patient material for mutations is now possible using methods such as chemical cleavage of mismatches (Cotton *et al., Proc. Natl. Acad. Sci. USA* 85:4397-4401, 1985; Montandon *et al., Nucleic Acids Res.* 9:3347-3358, 1989) and single-strand conformational polymorphism analysis (Orita *et al., Genomics* 5:874-879, 1989).

Please replace the paragraph beginning on page 52, line 18 with the following paragraph:

Alternatively, DNA extracted from a biological sample may be used directly for amplification. Direct amplification from genomic DNA would be appropriate for analysis of the entire *Mater* gene including regulatory sequences located upstream and downstream from the open reading frame, or intron/exon borders (see Table 2). By way of example, the intro-exon boundaries themselves can serve as sequences for oligonucleotide primers (or portions thereof) for us in *in vitro* amplification of such samples; representative examples of such oligonucleotides are shown in SEQ ID NOs: 25-~~38~~ 53. Reviews of direct DNA diagnosis have been presented by Caskey (*Science* 236:1223-1228, 1989) and by Landegren *et al.* (*Science* 242:229-237, 1989).

Please replace the paragraph beginning on page 53, line 3 with the following paragraph:

The detection of specific DNA mutations may be achieved by methods such as hybridization using allele specific oligonucleotides (ASOs) (Wallace *et al.,* CSHL Symp. Quant. Biol. 51:257-261, 1986), oligonucleotides specific for intron-exon boundaries (*e.g.*, any one of SEQ ID NOs: 25-~~38~~ 53), direct DNA sequencing (Church and Gilbert, *Proc. Natl. Acad. Sci. USA* 81:1991-1995, 1988), the use of restriction enzymes (Flavell *et al., Cell* 15:25-41, 1978; Geever *et al.*, 1981), discrimination on the basis of electrophoretic mobility in gels with denaturing reagent (Myers and Maniatis, Cold Spring Harbor Symp. Quant. Biol. 51:275-284, 1986), RNase protection (Myers *et al., Science* 230:1242-1246, 1985), chemical cleavage (Cotton *et al., Proc. Natl. Acad. Sci. USA* 85:4397-4401, 1985), and the ligase-mediated detection procedure (Landegren *et al., Science* 241:1077-1080, 1988).

Replace Sequence Listing

Please enter in the file the enclosed computer-readable form (submitted on 3.5 inch diskette) and paper copy of the Sequence Listing (33 pages), replacing all existing computer-readable forms and paper copies of the Sequence Listing previously submitted.

Statement In Compliance With 37 C.F.R. § 1.821(f)

In compliance with 37 C.F.R. § 1.821(f), the undersigned declares that the nucleotide and/or amino acid sequences presented in the paper copy of the "Sequence Listing" submitted herewith are the same as the sequences contained in the computer-readable form of the "Sequence Listing."